

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10
(B) CLONE: 1691243

009760 85526660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	
				5					10					15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	
				20					25					30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu	
				35					40					45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu	
				50					55					60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	
				65					70					75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	
				80					85					90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	
				95					100					105	
Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
				110					115					120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln	
				125					130					135	
Leu	Cys	Arg	Tyr	Pro	Asp										
				140											

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val	
				5					10					15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe	
				20					25					30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met	
				35					40					45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met	
				50					55					60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val	
				65					70					75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met	
				80					85					90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro	
				95					100					105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg	
				110					115					120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp	
				125					130					135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val	
				140					145					150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile	

His Ser Ile Trp	155	His Met Leu Ile Ala	160	Gly Ser Val Gly Phe	165
Leu Pro Pro Arg	170	Ala Lys Thr Asp His	175	Val Pro Ser Gly Ala	180
Arg Ala Arg Gly	185	Cys Gly Tyr Gln Leu	190	Cys Ile Asn Glu Gln	195
Glu Pro Gly Pro	200	Arg Gly Pro Arg Arg	205	Gly His Cys Gln Gln	210
Leu Cys Gln Leu	215	Arg Gly Ala Leu Gly	220	Ala Leu Arg Gly Tyr	225
Glu Cys Phe Leu	230	Glu Phe Phe Leu Gly	235	Val Trp Ser Pro Leu	240
Arg Arg Gln Ala	245	Val Phe Leu Glu Asp	250	Met Glu Ser Phe Ser	255
Thr Gln Asn Ser	260	Ser Arg Asp Leu Glu	265	Phe Pro Gly His Gly	270
Glu Leu Pro Glu	275	Gly Leu Glu Ser Pro	280	Cys Ile Met Glu Ser	285
Leu Arg Thr Gly	290	Ala Tyr Ala Gly Thr	295	Glu Ser Leu Arg Thr	300
Glu Ser Leu Leu	305	Gln Val Trp Ser Leu	310	Ser Trp Asp Ala Glu	315
Ser Gln Asp Met	320	Asp Ser Phe Pro Gly	325	Arg Gln Ser Pro Val	330
Ser Thr Ala Ser	335	Phe Gln Arg Arg Trp	340	Ser Leu Ser Trp Gly	345
Gln Ile Ser Arg	350	Phe Ser Gln Arg Leu	355	Ser Asn Ser Gly Leu	360
Leu Pro Ser Gln	365	Arg Gln Arg Leu Gly	370	Cys Ala Val Leu Trp	375
Arg Asp Cys Arg	380	Met Asp Gly Ala Gly	385	Thr Gly Ala Val Trp	390
Ala Gly Ile Leu	395	Val	400		405
	410				

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: PROSTUT10
 - (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAGG AGATTTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60
ATTACTAAGT TTTTCTTCG CTATGGTCCA TGTTGCCTAC AGCCTCTGCT TACCGATGAG 120
AAGGTCAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTTTCATG CAAATATTGA 180
AAACTCTTGG AATGAGGAAG AAGTTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240
GAGCCTTGGC TTA CTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300
AAACTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360
TACTTTCCAT GTTTTAATTT ATGGATGGAA ACGAGCTTTT GAGGAAGAGT ACTACAGATT 420
TTATACACCA CCAAACCTTG TTCTTGCTCT TGTTTTGCC TCAATTGTAA TTCTGGATCT 480

TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAAGCTGGA ATTTGTCTTC CTATTGACTC 540
TACTTCTTTA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGACAGT TAGGTGTACA 600
TGTGACTGAG TGTGGGCCAG TGAGATGAAG TCTCCTCAAA GGAAGGCAGC ATGTGTCCTT 660
TTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720
CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTA GAGACCAGAA AGACCTTGAC 780
TACTTCCCTA CTTCCACTGC TTTTTCCTGC ATTTAAGCCA TTGTAAATCT GGGTGTGTTA 840
CATGAAGTGA AAATTAATTC TTTCTGCCCT TCAGTTCTTT ATCCTGATAC CATTTAACAC 900
TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTTGAA AGCTTTTAAA GGATAATGTG 960
CAATTCACAT TAAAATTGAT TTTCCATTGT CAATTAGTTA TACTCATTTT CCTGCCTTGA 1020
TCTTTCATTA GATATTTTGT ATCTGCTTGG AATATATTAT CTTCTTTTAA ACTGTGTAAT 1080
TGGTAATTAC TAAAACTCTG TAATCTCCAA AATATTGCTA TCAAATTACA CACCATGTTT 1140
TCTATCATTC TCATAGATCT GCCTTATAAA CATTTAAATA AAAAGTACTA TTTAATGATT 1200
TAAAAAAA AA 1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
(B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCTGGGCC 60
ATTCGGAGTC GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120
TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTCT GCATCATGGA CTACGATGTG 180
CTGCAGTTCT GTGATTTCTT GGGCTCCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240
GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTTGC TGGGAGCTAT GCTGCTGTCC 300
ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTTCGCC 360
CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGGCA CTGCTACCCA 420
CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGC AGGCAGTGCC 480
GTCCTGCTTT ATGCTTTTGT GGAGACCCGG GACAACACT TCTACATTCA CAGCATTTGG 540
CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCC CTCGTGCCAA GACTGACCAC 600
GGGGTCCCAT CTGGAGCCCG GGCCCGGGGC TGTGGTTACC AGCTATGCAT CAACGAGCAG 660
GAGGAGCCTG GGCTTCGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720
AGAGGGGCTT TGGGCTTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780
GTGTGGAGCC CTCTTAGAAG GAGACAGGCT GTATTTCTTG AGGACATGGA GTCTTTCTCA 840
AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCTTGAG 900
GGCCTGGAGT CCCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960
GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTTCCTG GGATGCAGAG 1020
CCTTCCCAAG ACATGGATTC CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080
TTCCAGAGGA GGTGGAGTCT ATCTTGGGGA AACCAAATTT CCAGATTTTC CCAGAGGCTC 1140
AGCAACTCTG GCCTCAGGCT TCCTTCCCAG AGGCAGCGTC TGGGCTGTGC TGTGCTGTGG 1200
AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260
GTTTGATACA GGTGGAGTCT CTGTGTCTCC ATAGAAG 1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Gly	Leu	Leu	Leu	
				5					10					15	
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr	Ser	
				20					25					30	
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro	Asn	
				35					40					45	
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln	Ser	
				50					55					60	
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu	Tyr	
				65					70					75	
Cys															

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile	
				5					10					15	
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu	
				20					25					30	
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg	
				35					40					45	
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	
				50					55					60	
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu	
				65					70					75	
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe	
				80					85					90	
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu	
				95					100					105	
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala	
				125					130					135	
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr	
				140					145					150	
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe	
				155					160					165	
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser	
				170					175					180	
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe	
				185					190					195	

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Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser	
				200					205					210	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly	
				215					220					225	
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro	
				230					235					240	
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp	
				245					250					255	
Thr	Ile	Val	Ala	Asn	Pro										
				260											

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys	
				5					10					15	
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser	
				20					25					30	
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val	
				35					40					45	
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln	
				50					55					60	
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg	
				65					70					75	
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly	
				80					85					90	
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln	
				95					100					105	
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln	
				110					115					120	
Met	Gln	Phe	Leu	Glu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His	
				125					130					135	
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro	
				140					145					150	
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly	
				155					160					165	
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro	
				170					175					180	
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu	
				185					190					195	
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg	
				200					205					210	
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr	
				215					220					225	
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala	
				230					235					240	
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val	

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	245		250		255
Asp Glu Val His	Gly Asn Leu Leu Val	Val Asp Gln Thr Lys	Ser		
	260		265		270
Ser Asn Val Trp	Ser Leu Gly Val Thr	Ile Trp Glu Leu Phe	Glu		
	275		280		285
Leu Gly Ala Gln	Pro Tyr Pro Gln His	Ser Asp Arg Gln Val	Leu		
	290		295		300
Ala Tyr Ala Val	Arg Glu Gln Gln Leu	Lys Leu Pro Lys Pro	Gln		
	305		310		315
Leu Gln Leu Ala	Leu Ser Asp Arg Trp	Tyr Glu Val Met Gln	Phe		
	320		325		330
Cys Trp Leu Gln	Pro Glu Gln Arg Pro	Thr Ala Glu Glu Val	His		
	335		340		345
Leu Leu Leu Ser	Tyr Leu Cys Ala Lys	Gly Thr Thr Glu Leu	Glu		
	350		355		360
Glu Glu Phe Glu	Arg Arg Trp Arg Ser	Leu Arg Pro Gly Gly	Ser		
	365		370		375
Thr Gly Leu Gly	Ser Gly Ser Ala Ala	Pro Ala Ala Ala Thr	Ala		
	380		385		390
Ala Ser Ala Glu	Leu Thr Ala Ala Ser	Ser Phe Pro Leu Leu	Glu		
	395		400		405
Arg Phe Thr Ser	Asp Gly Phe His Val	Asp Ser Asp Asp Val	Leu		
	410		415		420
Thr Val Thr Glu	Thr Ser His Gly Leu	Asn Phe Glu Tyr Lys	Trp		
	425		430		435
Glu Ala Gly Cys	Gly Ala Glu Glu Tyr	Pro Pro Ser Gly Ala	Ala		
	440		445		450
Ser Ser Pro Gly	Ser Ala Ala Arg Leu	Gln Glu Leu Cys Ala	Pro		
	455		460		465
Asp Ser Ser Pro	Pro Gly Val Val Pro	Val Leu Ser Ala His	Ser		
	470		475		480
Pro Ser Val Gly	Ser Glu Tyr Phe Ile	Arg Leu Glu Gly Ala	Val		
	485		490		495
Pro Ala Ala Gly	His Asp Pro Asp Cys	Ala Gly Cys Ala Pro	Ser		
	500		505		510
Pro Gln Ala Val	Thr Asp Gln Asp Asn	Asn Ser Glu Glu Ser	Thr		
	515		520		525
Val Ala Ser Leu	Ala Met Glu Pro Leu	Leu Gly His Ala Pro	Pro		
	530		535		540
Thr Glu Gly Leu	Trp Gly Pro Cys Asp	His His Ser His Arg	Arg		
	545		550		555
Gln Gly Ser Pro	Cys Pro Ser Arg Ser	Pro Ser Pro Gly Thr	Pro		
	560		565		570
Met Leu Pro Ala	Glu Asp Ile Asp Trp	Gly Val Ala Thr Phe	Cys		
	575		580		585
Pro Pro Phe Phe	Asp Asp Pro Leu Gly	Ala Ser Pro Ser Gly	Ser		
	590		595		600
Pro Gly Ala Gln	Pro Ser Pro Ser Asp	Glu Glu Pro Glu Glu	Gly		
	605		610		615
Lys Val Gly Leu	Ala Ala Gln Cys Gly	His Trp Ser Ser Asn	Met		
	620		625		630
Ser Ala Asn Asn	Asn Ser Ala Ser Arg	Asp Pro Glu Ser Trp	Asp		
	635		640		645
Pro Gly Tyr Val	Ser Ser Phe Thr Asp	Ser Tyr Arg Asp Asp	Cys		
	650		655		660
Ser Ser Leu Glu	Gln Thr Pro Arg Ala	Ser Pro Glu Val Gly	His		
	665		670		675
Leu Leu Ser Gln	Glu Asp Pro Arg Asp	Phe Leu Pro Gly Leu	Val		
	680		685		690
Ala Val Ser Pro	Gly Gln Glu Pro Ser	Arg Pro Phe Asn Leu	Leu		
	695		700		705

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Pro	Leu	Cys	Pro	Ala	Lys	Gly	Leu	Ala	Pro	Ala	Ala	Cys	Leu	Ile
				710					715					720
Thr	Ser	Pro	Trp	Thr	Glu	Gly	Ala	Val	Gly	Gly	Ala	Glu	Asn	Pro
				725					730					735
Ile	Val	Glu	Pro	Lys	Leu	Ala	Gln	Glu	Ala	Glu	Gly	Ser	Ala	Glu
				740					745					750
Pro	Gln	Leu	Pro	Leu	Pro	Ser	Val	Pro	Ser	Pro	Ser	Cys	Glu	Gly
				755					760					765
Ala	Ser	Leu	Pro	Ser	Glu	Glu	Ala	Ser	Ala	Pro	Asp	Ile	Leu	Pro
				770					775					780
Ala	Ser	Pro	Thr	Pro	Ala	Ala	Gly	Ser	Trp	Val	Thr	Val	Pro	Glu
				785					790					795
Pro	Ala	Pro	Thr	Leu	Glu	Ser	Ser	Gly	Ser	Ser	Leu	Gly	Gln	Glu
				800					805					810
Ala	Pro	Ser	Ser	Glu	Asp	Glu	Asp	Thr	Thr	Glu	Ala	Thr	Ser	Gly
				815					820					825
Val	Phe	Thr	Asp	Leu	Ser	Ser	Asp	Gly	Pro	His	Thr	Glu	Lys	Ser
				830					835					840
Gly	Ile	Val	Pro	Ala	Leu	Arg	Ser	Leu	Gln	Lys	Gln	Val	Gly	Thr
				845					850					855
Pro	Asp	Ser	Leu	Asp	Ser	Leu	Asp	Ile	Pro	Ser	Ser	Ala	Ser	Asp
				860					865					870
Gly	Gly	Cys	Glu	Val	Leu	Ser	Pro	Ser	Ala	Ala	Gly	Pro	Pro	Gly
				875					880					885
Gly	Gln	Pro	Arg	Ala	Val	Asp	Ser	Gly	Tyr	Asp	Thr	Glu	Asn	Tyr
				890					895					900
Glu	Ser	Pro	Glu	Phe	Val	Leu	Lys	Glu	Ala	His	Glu	Ser	Ser	Glu
				905					910					915
Pro	Glu	Ala	Phe	Gly	Glu	Pro	Ala	Ser	Glu	Gly	Glu	Ser	Pro	Gly
				920					925					930
Pro	Asp	Pro	Leu	Leu	Ser	Val	Ser	Leu	Gly	Gly	Leu	Ser	Lys	Lys
				935					940					945
Ser	Pro	Tyr	Arg	Asp	Ser	Ala	Tyr	Phe	Ser	Asp	Leu	Asp	Ala	Glu
				950					955					960
Ser	Glu	Pro	Thr	Phe	Gly	Pro	Glu	Lys	His	Ser	Gly	Ile	Gln	Asp
				965					970					975
Ser	Gln	Lys	Glu	Gln	Asp	Leu	Arg	Ser	Pro	Pro	Ser	Pro	Gly	His
				980					985					990
Gln	Ser	Val	Gln	Ala	Phe	Pro	Arg	Ser	Ala	Val	Ser	Ser	Glu	Val
				995					1000					1005
Leu	Ser	Pro	Pro	Gln	Gln	Ser	Glu	Glu	Pro	Leu	Pro	Glu	Val	Pro
				1010					1015					1020
Arg	Pro	Glu	Pro	Leu	Gly	Ala	Gln	Gly	Pro	Val	Gly	Val	Gln	Pro
				1025					1030					1035
Val	Pro	Gly	Pro	Ser	His	Ser	Lys	Cys	Phe	Pro	Leu	Thr	Ser	Val
				1040					1045					1050
Pro	Leu	Ile	Ser	Glu	Gly	Ser	Gly	Thr	Glu	Pro	Gln	Gly	Pro	Ser
				1055					1060					1065
Gly	Gln	Leu	Ser	Gly	Arg	Ala	Gln	Gln	Gly	Gln	Met	Gly	Asn	Pro
				1070					1075					1080
Ser	Thr	Pro	Arg	Ser	Pro	Leu	Cys	Leu	Ala	Leu	Pro	Gly	His	Pro
				1085					1090					1095
Gly	Ala	Leu	Glu	Gly	Arg	Pro	Glu	Glu	Asp	Glu	Asp	Thr	Glu	Asp
				1100					1105					1110
Ser	Glu	Glu	Ser	Asp	Glu	Glu	Leu	Arg	Cys	Tyr	Ser	Val	Gln	Glu
				1115					1120					1125
Pro	Ser	Glu	Asp	Ser	Glu	Glu	Glu	Pro	Pro	Ala	Val	Pro	Val	Val
				1130					1135					1140
Val	Ala	Glu	Ser	Gln	Ser	Ala	Arg	Asn	Leu	Arg	Ser	Leu	Leu	Lys
				1145					1150					1155
Met	Pro	Ser	Leu	Leu	Ser	Glu	Ala	Phe	Cys	Asp	Asp	Leu	Glu	Arg

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	1160		1165		1170
Lys Lys Lys Ala Val	Ser Phe Phe Asp Asp	Val Thr Val Tyr Leu			
	1175		1180		1185
Phe Asp Gln Glu Ser	Pro Thr Arg Glu Thr	Gly Glu Pro Phe Pro			
	1190		1195		1200
Ser Thr Lys Glu Ser	Leu Pro Thr Phe Leu	Glu Gly Gly Pro Ser			
	1205		1210		1215
Ser Pro Ser Ala Thr	Gly Leu Pro Leu Arg	Ala Gly His Ser Pro			
	1220		1225		1230
Asp Ser Ser Ala Pro	Glu Pro Gly Ser Arg	Phe Glu Trp Asp Gly			
	1235		1240		1245
Asp Phe Pro Leu Val	Pro Gly Lys Ala Ala	Leu Val Thr Glu Leu			
	1250		1255		1260
Asp Pro Ala Asp Pro	Val Leu Ala Ala Pro	Pro Thr Pro Ala Ala			
	1265		1270		1275
Pro Phe Ser Arg Phe	Thr Val Ser Pro Thr	Pro Ala Ser Arg Phe			
	1280		1285		1290
Ser Ile Thr His Ile	Ser Asp Ser Asp Ala	Gln Ser Val Gly Gly			
	1295		1300		1305
Pro Ala Ala Gly Ala	Gly Gly Arg Tyr Thr	Glu Ala			
	1310		1315		

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